THE COLUMN COLUMN STATE OF THE STATE OF THE

HE BAND WITH BLUE AND AND BLUE WITH

GLL Ala Val GCT ATG Ser Met AGI

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-29

99 CTGLeu Ser GGA ATG Gly Met Phe CTC CTC CTC TTA Leu Leu Leu Leu Leu CTT $_{
m LLC}$ Phe Ser GIT AGT Val AGA

TGT ACC TTA AAC Leu Asn Cys Thr GCC AAG GCT Asp Ala Lys Ala -1 ↑ 1 GAT GCA Ala GAA CAT Glu His AGC AAT GTG Asn Val Ser Val Leu

114

GAA AAG Glu Glu Lys GAA TCASer TGC CCG CGT Cys Pro Arg ${\tt GLL}$ Val 15 Gly. GGA TyrCCA AGA ATT GCC TAT Ala Ile Arg 10

Pro .

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162

Cys $_{\mathrm{TGT}}$ Gly CGG ATA TGC ACC AAC TGT TGC GCA GGC ACG AAG GGT Lys \mathtt{Thr} G1yAla Cys Cys Asn Cys Ile

Arg

Asp 25

Asn

GAA GGA GAG TCT GAT Ser Glu Gly Glu GTT TGT CysVal GAT GAT GGA ACT TTT Thr: Phe Asp Asp Gly

Figure 1a

Ser

Phe

TIC AGI

TAC

TSMAN O.G. FIG. SUBC	STYSS 4	402	2/21	864 864 864 864 864 864 864 864 864 864	546	B
AGA AAT CCA AAG GCT TGT ACC TTA AAC TGT GAT CCA AGA	Pro Lys Ala Cys Thr Leu Asn Cys Asp Pro Arg Ile 65 TGC CCG CGT TCA GAA GAA AAG AAG AAT GAT CGG ATA 75 TSC CCG CGT TCA GAA GAA AAG AAG AAT GAT CGG ATA 75 80 80	ACC AAC TGT TGC GCA GGC ACG AAG GGT TGT AAG TAC TTC AGT GAT GAT Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys Lys Tyr Phe Ser Asp Asp 90	ACT	TGT CCT CGG AAT TGC GAT CCA AGA ATT GCC TAT GGG ATT TGC CCA CTT Cys Pro Arg Asp Pro Arg Ile Ala Tyr Gly Ile Cys Pro Leu 120	GCA GAA AAG AAG AAT GAT CGG ATA TGC ACC AAC TGT TGC GCA GGC Ala Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly 135	Figure 1b

	O.G. FIG.			
BY	CLASS	SUBCLASS		
DRAFTSMAN				

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B	642	069	738	786	834
. ACT TTT GTT TGT GAA Thr Phe Val Cys Glu 165	CCT CGG AAT TGT GAT Pro Arg Asn Cys Asp	GAA GAA AAG AAG AAT Glu Glu Lys Lys Asn 195	AAG GGT TGT AAG TAC Lys Gly Cys Lys Tyr 210	GAG TCT GAT CCT AAA Glu Ser Asp Pro Lys 230	AGA ATT GCC TAT GGG Arg ile Ala Tyr Gly 245
C TTT AGT GAT GAT GGA r Phe Ser Asp Asp Gly 160	A AAT CCA AAG GCC TGT s Asn Pro Lys Ala Cys 175	ATT TIIO C	TGC TGC GCA GGC AAA Cys Cys Ala Gly Lys 205	TTT GTT TGT GAA GGA Phe Val Cys Glu Gly 225	CGG AAT TGT GAT GGA Arg Asn Cys Asp Gly 240
AAA AAG GGT TGT AAG TAC Lys Lys Gly Cys Lys Tyr 155	GGA GAG TCT GAT CCT AAA Gly Gly Ser Asp Pro Lys 170	GGA AGA ATT GCC TAT GGG Gly Arg ile Ala Tyr Gly 185	GAT CGG ATA TGC ACC AAC Asp Arg Ile Cys Thr Asn 200	TTT AGT GAT GAT GGA ACT Phe Ser Asp Asp Gly Thr 215	AAT CCA AAG GCT TGT CCT Asn Pro Lys Ala Cys Pro 235

Figure 1c

APPROVED	O.G. FIG.			
BY	CLASS SUBCLASS			
DRAFTSMAN				
DRAFTSMAN				

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	882	930	978	1026	1074	1122
	ATT TGC CCA CTT TCA GAA GAA AAG AAG AAT GAT CGG ATA TGC ACA AAC Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn 250	TGT TGC GCA GGC AAA AAG GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr 265	TTT GTT TGT GAA GGA GAG TCT GAT CCT AGA AAT CCA AAG GCC TGT CCT Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Als Cys Pro 280	CGG AAT TGT GAT GGA AGA ATT GCC TAT GGA ATT TGC CCA CTT TCA GAA Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu 305	GAA AAG AAT GAT CGG ATA TGC ACC AAT TGT TGC GCA GGC AAG AAG Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys 315	GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT ATT TGT GAA GGA GAA Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Ile Cys Glu Gly Glu 330
J						

Figure 1d

1170	1220	1280	1340	1360
TCT GAA TAT GCC AGC AAA GTG GAT GAA TAT GTT GGT GAA GTG GAG AAT Aer Glu Tyr Ala Ser Lys Val Asp Glu Tyr Val Gly Glu Val Glu Asn 345	GAT CTC CAG AAG TCT AAG GTT GCT GTT TCC TAAGTCCTAA CTAATAATAT Asp Leu Gln Lys Ser Lys Val Ala Val Ser 360	GTAGTCTATG TATGAAACAA AGGCATGCCA ATATGCTCTG TCTTGCCTGT AATCTGTAAT	ATGGTAGTGG AGCTTTTCCA CTGCCTGTTT AATAAGAAAT GGAGCACTAG TTTGTTTTAG	TTAAAAAAA AAAAAAAA

Figure 1e

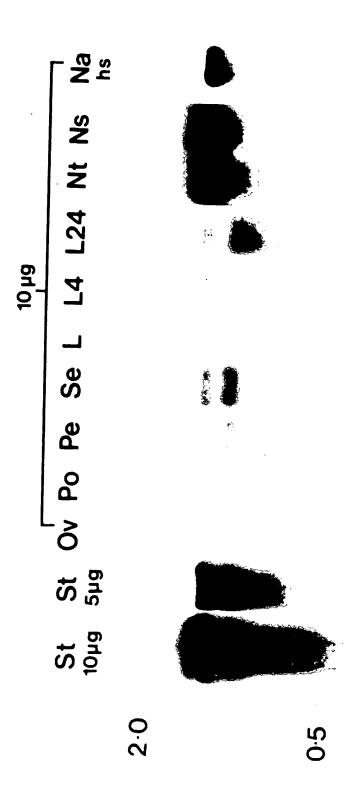


Figure 2

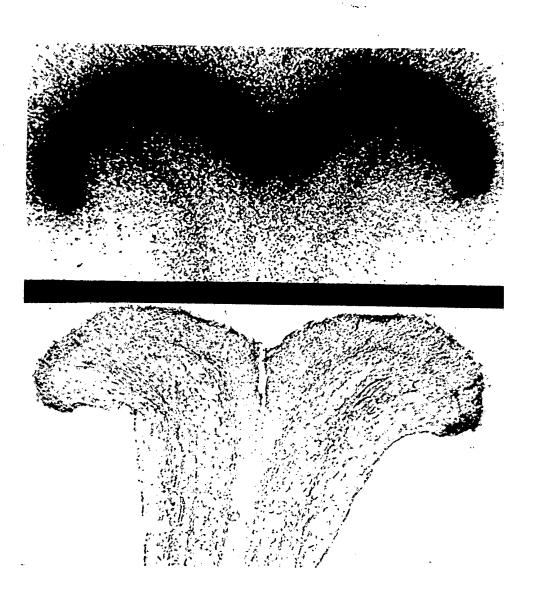


Figure 3

EcoRI HindIII



6.5

4.3

2·3 2·0

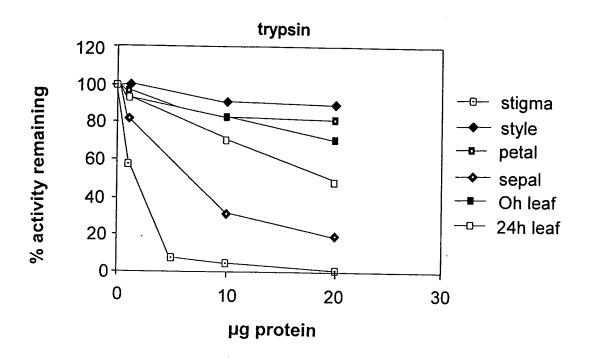


Figure 5a

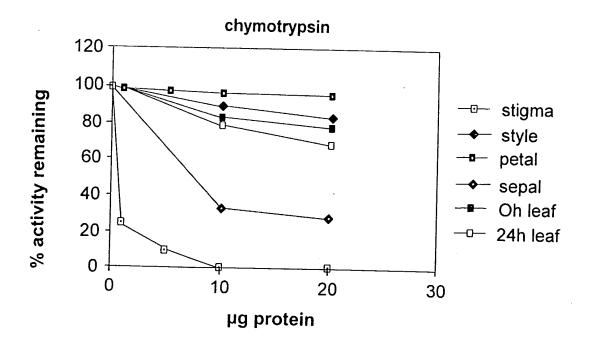


Figure 5b

Figure 6a

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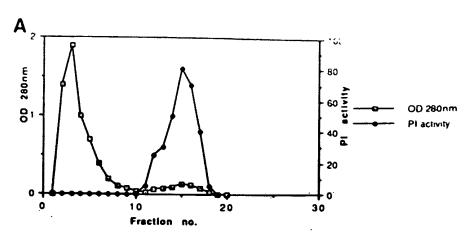
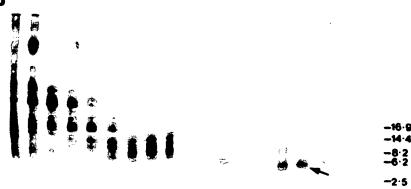


Figure 6b

B

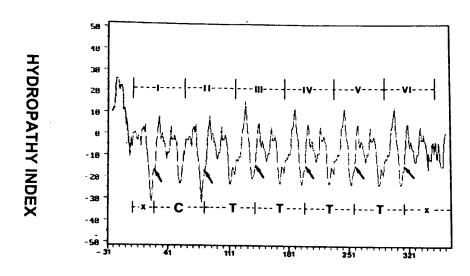


1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Figure 6c

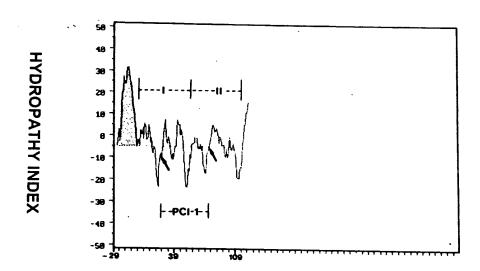
C

1 2 3



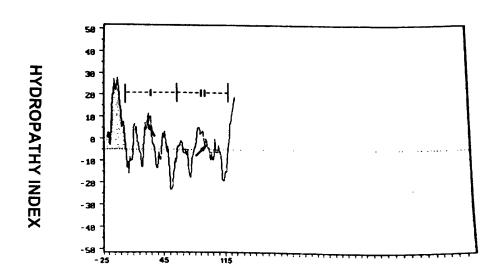
AMINO ACID RESIDUE NUMBER

Figure 7a



AMINO ACID RESIDUE NUMBER

Figure 7 b



AMINO ACID RESIDUE NUMBER

Figure 7c

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Figure 8a

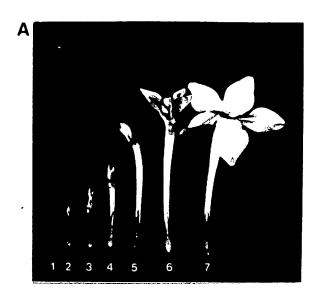
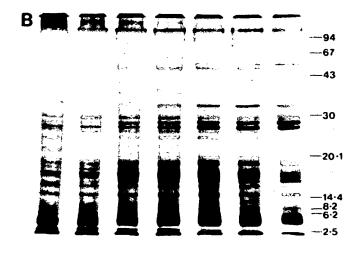
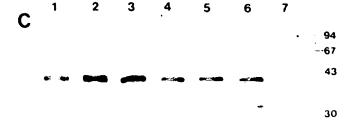


Figure 8b







14-4 8-2 6-2 2-5

20 -1

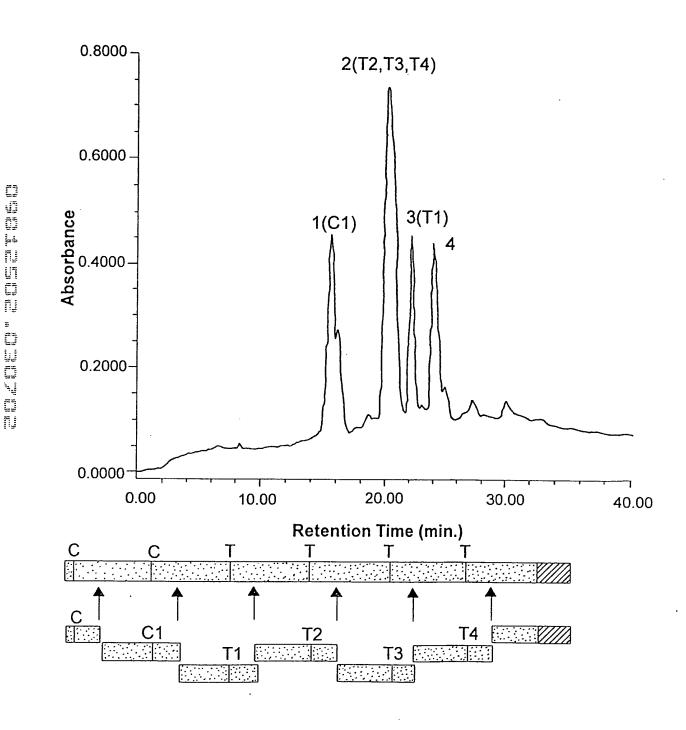


Figure 9a

DRICTNCCAGRAGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS DRICTNCCAGRAGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS DRICTNCCACKKGCKYFSDDGTFVCEGESDPRNPKACPRNCDCRIAYGICPLS DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRS DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPL 30 T3 **T**4 **T**2

Figure 9b

G (Tork) KG ر 2 U Z H U EKKNDRI 口 ICP(Rorl)(SorA)

Figure 10

1 2

Figure 11a

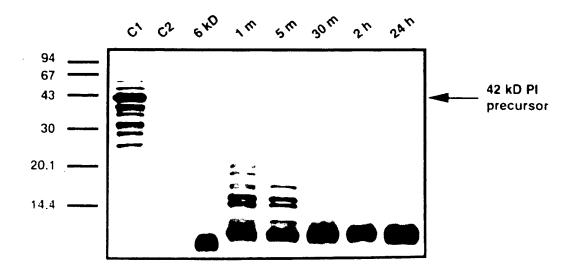


Figure 11 b

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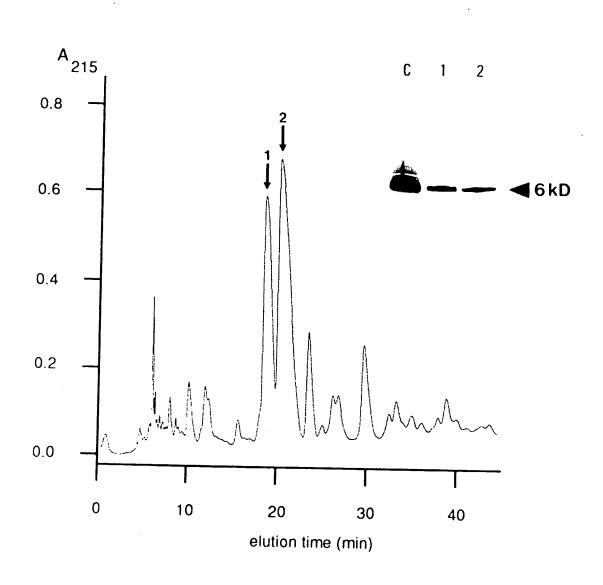


Figure 12

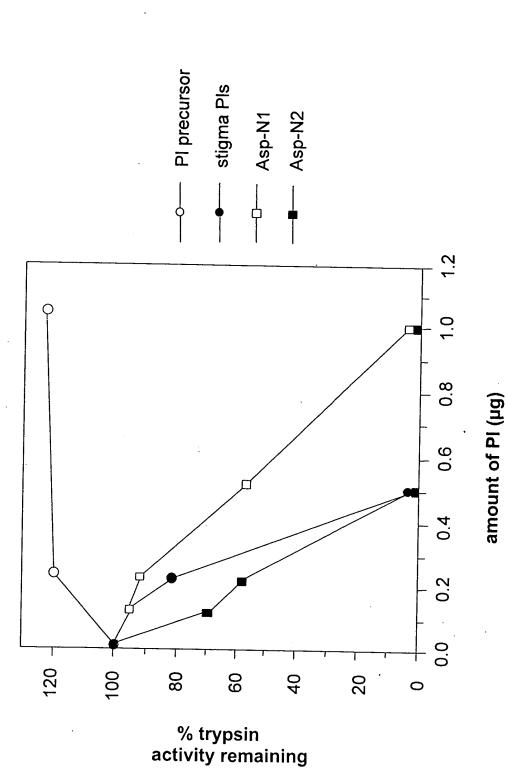


Figure 13a

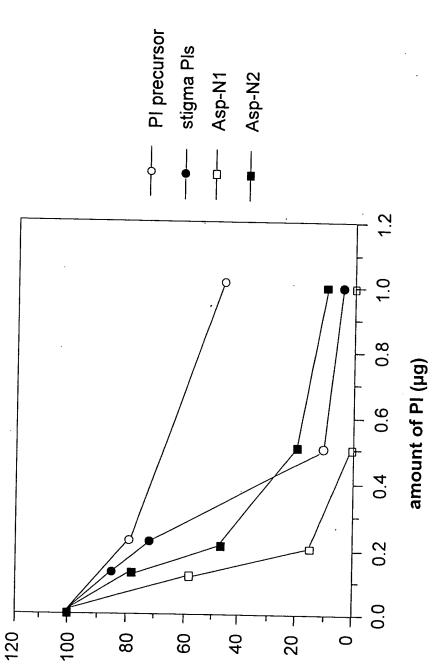


Figure 13b

% chymotrypsin activity remaining

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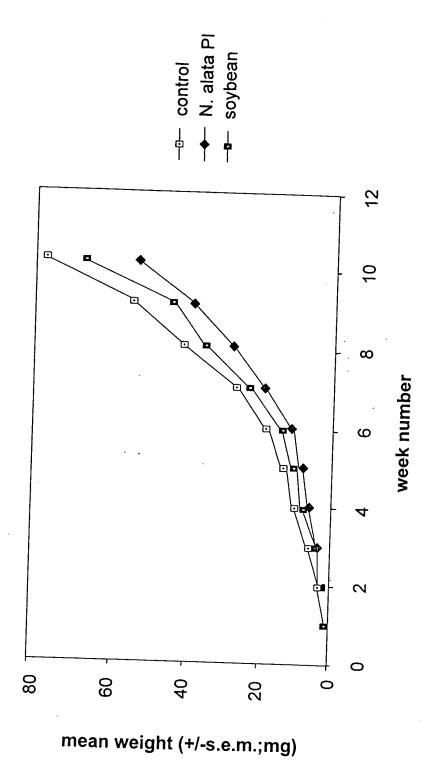


Figure 14